

17



1600

RAW SEQUENCE LISTING

DATE: 05/07/2003

PATENT APPLICATION: US/09/742,684A

TIME: 11:00:44

Input Set : A:\Slk17206.app

Output Set: N:\CRF4\05072003\I742684A.raw

3 <110> APPLICANT: MATHEWS, LAWRENCE S.
 4 VALE JR., WYLIE W.
 5 TSUCHIDA, KUNIHIRO
 7 <120> TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF RECEPTOR(S) OF
 8 THE ACTIVIN/TGF-BETA SUPERFAMILY
 10 <130> FILE REFERENCE: SALK1720-6
 12 <140> CURRENT APPLICATION NUMBER: 09/742,684A
 13 <141> CURRENT FILING DATE: 2000-12-19
 15 <150> PRIOR APPLICATION NUMBER: 08/476,123
 16 <151> PRIOR FILING DATE: 1995-06-07
 18 <150> PRIOR APPLICATION NUMBER: 08/300,584
 19 <151> PRIOR FILING DATE: 1994-09-02
 21 <150> PRIOR APPLICATION NUMBER: 07/880,220
 22 <151> PRIOR FILING DATE: 1992-05-08
 24 <150> PRIOR APPLICATION NUMBER: 07/773,229
 25 <151> PRIOR FILING DATE: 1991-10-09
 27 <150> PRIOR APPLICATION NUMBER: 07/698,709
 28 <151> PRIOR FILING DATE: 1991-05-10
 30 <160> NUMBER OF SEQ ID NOS: 16
 32 <170> SOFTWARE: PatentIn Ver. 2.1
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 36 <212> TYPE: DNA
 37 <213> ORGANISM: Mus sp.
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 41 <222> LOCATION: (71)..(1609)
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 47 Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu
 48 1 5 10
 50 atc tct tgc tct tca ggt gct ata ctt ggc aga tca gaa act cag gag 157
 51 Ile Ser Cys Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu
 52 15 20 25
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 55 Cys Leu Phe Phe Asn Ala Asn Trp Glu Arg Asp Arg Thr Asn Gln Thr
 56 30 35 40 45
 58 ggt gtt gaa cct tgc tat ggt gat aaa gat aaa cgg cga cat tgt ttt 253
 59 Gly Val Glu Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe
 60 50 55 60
 62 gct acc tgg aag aat att tct ggt tcc att gaa ata gtg aag caa ggt 301
 63 Ala Thr Trp Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly

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67	Cys Trp Leu Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Ile Glu			
68	80 85 90			
70	aaa aaa gac agc cct gaa gtg tac ttt tgt tgc tgt gag ggc aat atg	397		
71	Lys Lys Asp Ser Pro Glu Val Tyr Phe Cys Cys Glu Gly Asn Met			
72	95 100 105			
74	tgt aat gaa aag ttc tct tat ttt ccg gag atg gaa gtc aca cag ccc	445		
75	Cys Asn Glu Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro			
76	110 115 120 125			
78	act tca aat cct gtt aca ccg aag cca ccc tat tac aac att ctg ctg	493		
79	Thr Ser Asn Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu			
80	130 135 140			
82	tat tcc ttg gta cca cta atg tta att gca gga att gtc att tgt gca	541		
83	Tyr Ser Leu Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala			
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87	Phe Trp Val Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val			
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90	cct act caa gac cca gga cca ccc cca cct tcc cca tta cta ggg ttg	637		
91	Pro Thr Gln Asp Pro Gly Pro Pro Pro Ser Pro Leu Leu Gly Leu			
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95	Lys Pro Leu Gln Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys			
96	190 195 200 205			
98	gtc tgg aaa gcc cag ttg ctc aat gaa tat gtg gct gtc aaa ata ttt	733		
99	Val Trp Lys Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe			
100	210 215 220			
102	cca ata cag gac aaa cag tcc tgg cag aat gaa tat gaa gtc tat agt	781		
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111	Lys Arg Gly Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe			
112	255 260 265			
114	cat gaa aag ggc tca ctg tca gac ttt ctt aag gct aat gtg gtc tct	925		
115	His Glu Lys Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser			
116	270 275 280 285			
118	tgg aat gaa ctt tgt cat att gca gaa acc atg gct aga gga ttg gca	973		
119	Trp Asn Glu Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala			
120	290 295 300			
122	tat tta cat gag gat ata cct ggc tta aaa gat ggc cac aag cct gca	1021		
123	Tyr Leu His Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala			
124	305 310 315			
126	atc tct cac agg gac atc aaa agt aaa aat gtg ctg ttg aaa aac aat	1069		
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134 ggc aag tct gca ggt gac acc cat ggg cag gtt ggt acc cgg agg tat 1165
135 Gly Lys Ser Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr
136 350 355 360 365
138 atg gct cca gag gtg ttg gag ggt gct ata aac ttc caa agg gac gca 1213
139 Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala
140 370 375 380
142 ttt ctg agg ata gat atg tac gcc atg gga tta gtc cta tgg gaa ttg 1261
143 Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu
144 385 390 395
146 gct tct cgt tgc act gct gca gat gga ccc gta gat gag tac atg tta 1309
147 Ala Ser Arg Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu
148 400 405 410
150 cca ttt gag gaa gaa att ggc cag cat cca tct ctt gaa gat atg cag 1357
151 Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln
152 415 420 425
154 gaa gtt gtt gtg cat aaa aaa aag agg cct gtt tta aga gat tat tgg 1405
155 Glu Val Val Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp
156 430 435 440 445
158 cag aaa cat gca gga atg gca atg ctc tgt gaa acg ata gaa gaa tgt 1453
159 Gln Lys His Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys
160 450 455 460
162 tgg gat cat gat gca gaa gcc agg tta tca gct gga tgt gta ggt gaa 1501
163 Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu
164 465 470 475
166 aga att act cag atg caa aga cta aca aat atc att act aca gag gac 1549
167 Arg Ile Thr Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp
168 480 485 490
170 att gta aca gtg gtc aca atg gtg aca aat gtt gac ttt cct ccc aaa 1597
171 Ile Val Thr Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys
172 495 500 505
174 gaa tct agt cta tgatggtggc accgtctgta cacactgagg actgggactc 1649
175 Glu Ser Ser Leu
176 510
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223 Phe Asn Ala Asn Trp Glu Arg Asp Arg Thr Asn Gln Thr Gly Val Glu
224 35 40 45
226 Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
227 50 55 60
229 Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
230 65 70 75 80
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233 85 90 95
235 Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
236 100 105 110
238 Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn
239 115 120 125
241 Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu
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245 145 150 155 160
247 Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln
248 165 170 175
250 Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu
251 180 185 190
253 Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys
254 195 200 205
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257 210 215 220
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260 225 230 235 240
262 Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly
263 245 250 255
265 Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys
266 260 265 270
268 Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu
269 275 280 285
271 Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His
272 290 295 300
274 Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His
275 305 310 315 320
277 Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala

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Input Set : A:\Slk17206.app

Output Set: N:\CRF4\05072003\I742684A.raw

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286 Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
287          370          375          380
289 Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
290 385          390          395          400
292 Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
293          405          410          415
295 Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val
296          420          425          430
298 Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His
299          435          440          445
301 Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
302          450          455          460
304 Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
305 465          470          475          480
307 Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
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322 <221> NAME/KEY: CDS
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330 tgtgaagctg ctgctgcaga aggtggagtc gttgcatgag ggtgggggga gtcgctgctg 180
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334 actcgctttt aaccctttcc ctggcggagc ccacgcgtct ttcattccctc ctgccgcggc 300
336 cgctgagcga ccagagcgcg acattgttgc ggcgggggat tgggcgacat tgttgcaaat 360
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340 cgaatgggat tttatctgtg tcggtgagag aagcggatcc caggagc atg ggg gcg 476
341          Met Gly Ala
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345 Ser Val Ala Leu Thr Phe Leu Leu Leu Leu Ala Thr Phe Arg Ala Gly
346          5          10          15
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349 Ser Gly His Asp Glu Val Glu Thr Arg Glu Cys Ile Tyr Tyr Asn Ala
350 20          25          30          35
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/742,684A

DATE: 05/07/2003
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Input Set : A:\Slk17206.app
Output Set: N:\CRF4\05072003\I742684A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:10; Xaa Pos. 1,3,4,6
Seq#:13; N Pos. 11,14,17
Seq#:14; N Pos. 12,15,24,30,33
Seq#:15; N Pos. 346